

=====

Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2012; month=1; day=25; hr=9; min=7; sec=31; ms=11;]

=====

Reviewer Comments:

<210> 70

<211> 174

<212> PRT

<213> Oerskovia jenensis

<400> 70

(ERRORED PORTION SHOWN BELOW)

Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Leu Ala

115

120

125

Please remove the blank lines between the above amino acid numbers and their respective amino acids: amino acid numbers must appear directly below their amino acids.

<210> 125

<211> 189

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

(ERRORED PORTION SHOWN BELOW)

<220>

<221> VARIANT
<222> 1, 8-16, 24, 35, 36, 38, 39, 41-44, 48, 61-64, 66, 67, 69-71, 81, 87, 89, 93, 109-111, 113, 116
<223> Xaa can be any naturally occurring amino acid

The above "<222>" line exceeds the Sequence Rules' required 72-character line limit; please insert a hard return after "69-71,"; that way, the remaining response will move to the next line. See below for sample:

<220>
<221> VARIANT
<222> 1, 8-16, 24, 35, 36, 38, 39, 41-44, 48, 61-64, 66, 67, 69-71,
81, 87, 89, 93, 109-111, 113, 116
<223> Xaa can be any naturally occurring amino acid

<210> 134
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 134

(ERRORED PORTION SHOWN BELOW)

Val Asn Glu Arg Gly Glu Gln Val Gln Leu Lys Gly Met Ser Ser His

50

55

60

Please remove the blank lines between the above amino acid numbers and their respective amino acids. Amino acid numbers must appear directly below their amino acids.

<210> 639
<211> 255
<212> PRT

<213> Streptogrisin C

Regarding the above "<213> Streptogrisin": per Sequence Rules, the only valid "<213>" responses are: the Genus species of the organism, "Artificial Sequence", or "Unknown". "Artificial Sequence" and "Unknown" require an explanation in the "<220>-<223>" section; please clearly indicate the source of the genetic material. "Streptogrisin" also appears in subsequent sequences (as the "<213>" response).

<210> 640

<211> 185

<212> PRT

<213> Streptogrisin B

<400> 640

(see below)

Gly Phe Asn Val Arg Ser Gly Ser Thr Tyr Tyr Phe Leu Thr Ala Gly

20

25

30

Please check the above "<213>" response: as indicated in Sequence 639 above, the only valid "<213>" responses are: the Genus species of the organism, "Artificial Sequence", or "Unknown". "Artificial Sequence" and "Unknown" require explanation in the "<220>-<223>" section. Please remove the blank lines between the above amino acid numbers and their respective amino acids; amino acid numbers must appear directly below their amino acids.

<210> 642

<211> 188

<212> PRT

<213> Streptogrisin D

<400> 642

(see below)

Gly Gln Ala Val Thr Arg Ser Gly Ser Thr Thr Gln Val His Asp Gly

100

105

110

Please check "Streptogrisin" as the above "<213>" response. Please remove the blank lines between the above amino acid numbers and their amino acids. Amino acid numbers must appear directly below their amino acids.

To correct the sequence listing errors noted in this report - The recommended method for correction of errors is to access the sequence listing working file using the software program in which the listing was originally prepared, e.g., the project file in PatentIn, make any necessary corrections within that program, then generate a new sequence listing file. Use of a word processing program to correct errors directly in the original sequence listing file is strongly discouraged, since such programs often introduce unintended changes to the sequence listing, rendering the listing unacceptable. When the working file or original program is not available for correction, then use of a common or plain text-only editor, such as NotePad, to edit the original sequence listing file may suffice.

Application No: 10576331 Version No: 2.0

Input Set:

Output Set:

Started: 2012-01-24 13:57:36.425
Finished: 2012-01-24 13:57:58.381
Elapsed: 0 hr(s) 0 min(s) 21 sec(s) 956 ms
Total Warnings: 605
Total Errors: 28
No. of SeqIDs Defined: 656
Actual SeqID Count: 656

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 402	Undefined organism found in <213> in SEQ ID (5)
W 402	Undefined organism found in <213> in SEQ ID (6)
W 402	Undefined organism found in <213> in SEQ ID (7)
W 402	Undefined organism found in <213> in SEQ ID (8)
W 402	Undefined organism found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 402	Undefined organism found in <213> in SEQ ID (18)
W 402	Undefined organism found in <213> in SEQ ID (37)
W 402	Undefined organism found in <213> in SEQ ID (38)

Input Set:

Output Set:

Started: 2012-01-24 13:57:36.425
Finished: 2012-01-24 13:57:58.381
Elapsed: 0 hr(s) 0 min(s) 21 sec(s) 956 ms
Total Warnings: 605
Total Errors: 28
No. of SeqIDs Defined: 656
Actual SeqID Count: 656

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (40)
W 213	Artificial or Unknown found in <213> in SEQ ID (45)
W 213	Artificial or Unknown found in <213> in SEQ ID (46)
W 213	Artificial or Unknown found in <213> in SEQ ID (47)
W 213	Artificial or Unknown found in <213> in SEQ ID (48)
W 213	Artificial or Unknown found in <213> in SEQ ID (49)
W 213	Artificial or Unknown found in <213> in SEQ ID (50)
W 213	Artificial or Unknown found in <213> in SEQ ID (51)
W 213	Artificial or Unknown found in <213> in SEQ ID (52)
W 402	Undefined organism found in <213> in SEQ ID (61)
W 402	Undefined organism found in <213> in SEQ ID (62)
W 402	Undefined organism found in <213> in SEQ ID (65)
W 402	Undefined organism found in <213> in SEQ ID (66)
W 402	Undefined organism found in <213> in SEQ ID (69) This error has occurred more than 20 times, will not be displayed
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (70)
W 213	Artificial or Unknown found in <213> in SEQ ID (79)
W 213	Artificial or Unknown found in <213> in SEQ ID (80)
W 213	Artificial or Unknown found in <213> in SEQ ID (81)
W 213	Artificial or Unknown found in <213> in SEQ ID (82)
W 213	Artificial or Unknown found in <213> in SEQ ID (83)
W 213	Artificial or Unknown found in <213> in SEQ ID (84)

Input Set:

Output Set:

Started: 2012-01-24 13:57:36.425

Finished: 2012-01-24 13:57:58.381

Elapsed: 0 hr(s) 0 min(s) 21 sec(s) 956 ms

Total Warnings: 605

Total Errors: 28

No. of SeqIDs Defined: 656

Actual SeqID Count: 656

Error code	Error Description
E 341	'Xaa' position not defined SEQID (125) POS (170)
E 341	'Xaa' position not defined SEQID (125) POS (171)
E 341	'Xaa' position not defined SEQID (125) POS (172)
E 341	'Xaa' position not defined SEQID (125) POS (173)
E 341	'Xaa' position not defined SEQID (125) POS (174)
E 341	'Xaa' position not defined SEQID (125) POS (175)
E 341	'Xaa' position not defined SEQID (125) POS (176)
E 341	'Xaa' position not defined SEQID (125) POS (177)
E 341	'Xaa' position not defined SEQID (125) POS (178)
E 341	'Xaa' position not defined SEQID (125) POS (179)
E 341	'Xaa' position not defined SEQID (125) POS (180)
E 341	'Xaa' position not defined SEQID (125) POS (181)
E 341	'Xaa' position not defined SEQID (125) POS (182)
E 341	'Xaa' position not defined SEQID (125) POS (183)
E 341	'Xaa' position not defined SEQID (125) POS (184)
E 341	'Xaa' position not defined SEQID (125) POS (185)
E 341	'Xaa' position not defined SEQID (125) POS (186)
E 341	'Xaa' position not defined SEQID (125) POS (187)
E 341	'Xaa' position not defined SEQID (125) POS (188)
E 341	'Xaa' position not defined SEQID (125) POS (189) This error has occurred more than 20 times, will not be displayed
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (134)

Input Set:

Output Set:

Started: 2012-01-24 13:57:36.425
Finished: 2012-01-24 13:57:58.381
Elapsed: 0 hr(s) 0 min(s) 21 sec(s) 956 ms
Total Warnings: 605
Total Errors: 28
No. of SeqIDs Defined: 656
Actual SeqID Count: 656

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (640)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (642)

SEQUENCE LISTING

<110> Jones, Brian E.
Kolkman, Marc
Leefflang, Chris
Oh, Hiroshi
Poulose, A.J.
Sadlowski, Eugene S.
Shaw, Andrew
van der Kleij, Wilhelmus A.H.
van Marrenwijk, Leo

<120> Serine Proteases, Nucleic Acids Encoding Serine Enzymes and
Vectors and Host Cells Incorporating Same

<130> GC819-2-US/B

<140> 10576331
<141> 2012-01-24

<150> PCT/US2004/039066
<151> 2004-11-19

<150> US 60/523,609
<151> 2003-11-19

<160> 656

<170> PatentIn version 3.2

<210> 1
<211> 1680
<212> DNA
<213> Cellulomonas strain 69B4

<400> 1
g c g c g c t g c g c c c a c g a c g a c g c c g t c c g c c g t t c g c c g g c g t a c c t g c g t t g g c t c a c c 60
a c c c a c c a g a t c g a c c t c c a t a a c g a g g c c g t a t g a c c a g a a a g g g a t c t g c c a c c g c c c 120
a c c a g c a c g c t c c t a a c c t c c g a g c a c c g g c g a c c g c c g g t g c g a t g a a a g g g a c g a a c 180
c g a g a t g a c a c c a c g c a c a g t c a c g c g g g c c c t g g c c g t g g c c a c c g a g c c g c c a c a c t 240
c c t g g c a g g c g g c a t g g c c g c c c a g g c c a a c g a g c c c g c a c c a c c g g g a g c g c g a g c g c 300
a c c g c c a c g c c t g g c c g a g a g t c t g a c c c c g a c c t c c t c g a g g c c a t g g a g c g c g a c c t 360
g g g c c t c g a c g c g g a g g a a g c c g c g c c a c c c t g g c g t t c a g c a c g a c g c a g c c g a g a c 420
c g g c g a g g c c c t c g c c g a a g a g t c g a c g a c g a g g a c t t c g c c g g c a c t g g g t c g a g g a c g a 480
c g t c c t g t a c g t c g c c a c c a c g a c g a g g a c g c c g t c g a g a g g t c g a g g c g a a g g c g c 540
c a c g g c c g t c a c c g t c g a g c a c t c c c t g g c c g a c c t c g a g g c c t g g a a g a c c g t c c t c g a 600
c g c g c c c t c g a g g g c c a c g a c g t g c c a c c t g g t a c g t c g a c g t c c c g a c c a a c a g 660
c g t c g t c g t c g c c g t c a a g g c c g g a g c c c a g g a c g t c g c c g c c g g c c t c g t c g a a g g t g c 720
c g a c g t c c c g t c c g a c g c c g t g a c c t t c g t c g a g a c c g a c g a g a c c c c g c g g a c c a t g t t 780
c g a c g t g a t c g g c g g c a a c g c c t a c a c c a t c g g g g g g c g c a g c c g t g e t c g a t c g g g t t 840
c g c g g t c a a c g g c g g g t t c a t c a c c g c c g c c a c t g c g g c c g c a c c c g g c g c c a c c a c c g c 900
c a a c c c c a c c g g g a c c t t c g c c g g g t c c a g c t t c c c g g g c a a c g a c t a c g c g t t c g t c c g 960
t a c c g g g g c c g g c g t g a a c c t g c t g g c c c a g g t c a a c a a c t a c t c c g g t g g c c g c t c c a 1020
g g t c g c c g g g c a c a c c g c g g c c c c c g t c g g c t c g g c c g t g t g c c g g t c c g g g t c g a c c a c 1080
c g g g t g g c a c t g c g g c a c c a t c a c t g c g t c a a c t c c t c g g t c a c c t a c c c g a g g g c a c 1140
c g t c c g c g g c c t g a t c c g c a c c a c c g t c t g c g c c g a g c c c g g c g a c t c c g g t g g c t c g c t 1200

gtctgcgcggc	aaccaggccc	agggcggtcac	gtccggcggc	tccggcaact	gccgcaccgg	1260
tggcaccacg	ttcttccagc	cggtaacccc	catcctccag	gcgtacggcc	tgaggatgat	1320
caccacggac	tggggcagca	gccccggccc	tgcaccgacc	tcttgaccgc	gctacgcccg	1380
caccttcacc	gggaccctcg	cggccggccg	ggccgcgcgc	cagcccaacg	ggtcctacgt	1440
gcaggtcaac	cggtcgggga	cccacagcgt	gtgcctcaac	gggccctccg	gtgcggactt	1500
cgacctctac	gtgcagcgct	ggaacggcag	ctcctgggtg	accgtcgccc	agagcacctc	1560
ccccggctcc	aacgagacca	tcacctaccg	cggcaacgcc	ggctactacc	gctacgtggt	1620
caacgccgcg	tccggctccg	gtgcctacac	catggggctc	acctccccct	gacgtagcgc	1680

<210> 2

<211> 1488

<212> DNA

<213> Cellulomonas strain 69B4

<400> 2

atgacaccac	gcacagtcac	gcggggccctg	gccgtggcca	ccgcagccgc	cacactcctg	60
gcaggcggca	tggccgccc	ggccaacgag	ccgcaccac	ccgggagcgc	gagcgcaccg	120
ccacgcctgg	ccgagaagct	cgaccccgac	ctcctcgagg	ccatggagcg	cgacctgggc	180
ctcgacgcgg	aggaagccgc	cgccaccctg	gcgttccagc	acgacgcagc	cgagaccggc	240
gaggccctcg	ccgaagagct	cgacgaggac	ttcgccggca	cctgggtcga	ggacgacgtc	300
ctgtacgtcg	ccaccaccga	cgaggacgcc	gtcgaggagg	tcgagggcga	aggcgccacg	360
gccgtcaccg	tcgagcactc	cctggccgac	ctcgaggcct	ggaagaccgt	cctcgacgcc	420
gccctcgagg	gccacgacga	cgtgccacc	tggtagctcg	acgtcccgac	caacagcgtc	480
gtcgtcgccg	tcaaggcccg	agcccaggac	gtcgccgcgc	gcctcgtcga	aggtgccgac	540
gtcccgtccg	acgccgtgac	cttcgtcgag	accgacgaga	ccccgcggac	catgttcgac	600
gtgatcggcg	gcaacgccta	caccatcggg	gggcgcagcc	gctgctcgat	cgggttcgcg	660
gtcaacggcg	ggttcatacac	cgccggccac	tgcggccgca	ccggcgccac	caccgccaac	720
cccaccggga	ccttcgcccg	gtccagcttc	ccgggcaacg	actacgcgtt	cgtccgtacc	780
ggggccggcg	tgaacctgct	ggcccaggtc	aacaactact	ccggtggccg	cgtccaggtc	840
gccgggcaca	ccgcggcccc	cgtcggtctg	gccgtgtgcc	ggtccgggtc	gaccaccggg	900
tggcactgcg	gcaccatcac	tgcgtcaaac	tcctcggtca	cctaccccga	gggcaccgtc	960
cgccggcctga	tccgcaccac	cgtctgcgcc	gagcccgggc	actccgggtg	ctcgtgctc	1020
gccggcaacc	aggcccaggg	cgtcacgtcc	ggcggtccg	gcaactgccg	caccggtggc	1080
accacgttct	tccagccggg	caaccccatc	ctccaggcgt	acggcctgag	gatgatcacc	1140
acggactcgg	gcagcagccc	ggccctgca	ccgacctcct	gcaccggcta	cgcccgccac	1200
ttcaccggga	ccctcgccgg	cggccggggc	gccgcccagc	ccaacgggtc	ctacgtgcag	1260
gtcaaccggg	ccgggaccca	cagcgtgtgc	ctcaacgggc	cctccggtgc	ggacttcgac	1320
ctctacgtgc	agcgttgaa	cggcagctcc	tgggtgaccg	tcgcccagag	cacctcccc	1380
ggctccaacg	agaccatcac	ctaccgcggc	aacgcccggc	actaccgcta	cgtggtcaac	1440
gccgcgtccg	gtcgcgggtg	ctacaccatg	gggtcacccc	tcccctga		1488

<210> 3

<211> 1404

<212> DNA

<213> Cellulomonas spp.

<400> 3

aacgagcccc	caccaccccg	gagcgcgagc	gcaccgccac	gcctggccga	gaagctcgac	60
cccgaacctc	tcgaggccat	ggagcgcgac	ctgggcctcg	acgcggagga	agccgcgcgc	120
acctggcgt	tccagcacga	cgcagccgag	accggcgagg	ccctcgccga	agagctcgac	180
gaggacttcg	ccggcacctg	ggtcgaggac	gacgtcctgt	acgtcgccac	caccgacgag	240
gacgccgtcg	aggaggtcga	gggcgaaggc	gccacggccg	tcaccgtcga	gcactccctg	300
gccgaacctc	aggcctggaa	gaccgtcctc	gacgccgcgc	tcgagggcc	cgacgacgtg	360
cccacctggt	acgtcgacgt	cccgaacca	agcgtcgtcg	tcgccgtcaa	ggccggagcc	420
caggacgtcg	ccgcgggcct	cgtcgaagg	gccgacgtcc	cgtccgacgc	cgtgaccttc	480
gtcgagaccg	acgagacccc	gcggaccatg	ttcgacgtga	tcggcggcaa	cgctacacc	540
atcggggggc	gcagccgctg	ctcgatcggg	ttcgcggtca	acggcggggt	catcaccgcc	600

ggccactgcg	gccgcaccgg	cgccaccacc	gccaacccca	ccgggacctt	cgccgggtcc	660
agcttcccgg	gcaacgacta	cgcgttcgtc	cgtaaccggg	ccggcgtgaa	cctgctggcc	720
cagggtcaaca	actactccgg	tggccgcgtc	caggtcgcgc	ggcacaccgc	ggcccccgtc	780
ggctcggccg	tgtgccggtc	cgggtcgacc	accgggtggc	actgcggcac	catcactgcg	840
ctcaactcct	cggtcaccta	ccccgagggc	accgtccgcg	gcctgatccg	caccaccgtc	900
tgcgccgagc	ccggcgactc	cgggtggctcg	ctgctcgccg	gcaaccaggc	ccagggcgtc	960
acgtccggcg	gctccggcaa	ctgccgcacc	ggtggcacca	cgttcttcca	gccgggtcaac	1020
cccatectcc	aggcgtacgg	cctgaggatg	atcaccacgg	actcgggcag	cagcccggcc	1080
cctgcaccga	cctcctgcac	cggtacgcc	cgcaccttca	ccgggaccct	cgcggccggc	1140
cgggccgcgc	cccagcccaa	cgggtcctac	gtgcagggtca	accggtccgg	gacccacagc	1200
gtgtgcctca	acgggccctc	cgggtgccgg	ttcgacctct	acgtgcagcg	ctggaacggc	1260
agctcctggg	tgaccgtcgc	ccagagcacc	tccccgggct	ccaacgagac	catcacctac	1320
cgcggcaacg	ccggctacta	ccgctacgtg	gtcaacgcgc	cgtccggctc	cgggtgcctac	1380
accatggggc	tcaccctccc	ctga				1404

<210> 4
 <211> 567
 <212> DNA
 <213> Cellulomonas spp.

<400> 4						
ttcgacgtga	tcggcggcaa	cgcctacacc	atcggggggc	gcagccgctg	ctcgatcggg	60
ttcgcggtca	acggcggggt	catcaccgcc	ggccactgcg	gccgcaccgg	cgccaccacc	120
gccaacccca	ccgggacctt	cgccgggtcc	agcttcccgg	gcaacgacta	cgcgttcgtc	180
cgtaccgggg	ccggcgtgaa	cctgctggcc	cagggtcaaca	actactccgg	tggccgcgtc	240
caggtcgcgc	ggcacaccgc	ggcccccgtc	ggctcggcgc	tgtgccggtc	cgggtcgacc	300
accgggtggc	actgcggcac	catcactgcg	ctcaactcct	cggtcaccta	ccccgagggc	360
accgtccgcg	gcctgatccg	caccaccgtc	tgcgccgagc	ccggcgactc	cgggtggctcg	420
ctgctcgccg	gcaaccaggc	ccagggcgtc	acgtccggcg	gctccggcaa	ctgccgcacc	480
ggtggcacca	cgttcttcca	gccgggtcaac	cccatcctcc	aggcgtacgg	cctgaggatg	540
atcaccacgg	actcgggcag	cagcccc				567

<210> 5
 <211> 83
 <212> DNA
 <213> Cellulomonas strain 69B4

<400> 5						
atgacaccac	cacagtcacg	cgggccctgg	ccgtggccac	cgcagccgcc	acactcctgg	60
caggcggcat	ggccgccag	gcc				83

<210> 6
 <211> 495
 <212> PRT
 <213> Cellulomonas strain 69B4

<400> 6

Met	Thr	Pro	Arg	Thr	Val	Thr	Arg	Ala	Leu	Ala	Val	Ala	Thr	Ala	Ala
1				5					10					15	
Ala	Thr	Leu	Leu	Ala	Gly	Gly	Met	Ala	Ala	Gln	Ala	Asn	Glu	Pro	Ala
				20				25						30	
Pro	Pro	Gly	Ser	Ala	Ser	Ala	Pro	Pro	Arg	Leu	Ala	Glu	Lys	Leu	Asp
				35				40						45	
Pro	Asp	Leu	Leu	Glu	Ala	Met	Glu	Arg	Asp	Leu	Gly	Leu	Asp	Ala	Glu
				50				55						60	
Glu	Ala	Ala	Ala	Thr	Leu	Ala	Phe	Gln	His	Asp	Ala	Ala	Glu	Thr	Gly

65		70		75		80									
Glu	Ala	Leu	Ala	Glu	Glu	Leu	Asp	Glu	Asp	Phe	Ala	Gly	Thr	Trp	Val
		85						90						95	
Glu	Asp	Asp	Val	Leu	Tyr	Val	Ala	Thr	Thr	Asp	Glu	Asp	Ala	Val	Glu
		100						105					110		
Glu	Val	Glu	Gly	Glu	Gly	Ala	Thr	Ala	Val	Thr	Val	Glu	His	Ser	Leu
		115						120					125		
Ala	Asp	Leu	Glu	Ala	Trp	Lys	Thr	Val	Leu	Asp	Ala	Ala	Leu	Glu	Gly
		130						135					140		
His	Asp	Asp	Val	Pro	Thr	Trp	Tyr	Val	Asp	Val	Pro	Thr	Asn	Ser	Val
		145						150					155		160
Val	Val	Ala	Val	Lys	Ala	Gly	Ala	Gln	Asp	Val	Ala	Ala	Gly	Leu	Val
				165						170				175	
Glu	Gly	Ala	Asp	Val	Pro	Ser	Asp	Ala	Val	Thr	Phe	Val	Glu	Thr	Asp
				180						185				190	
Glu	Thr	Pro	Arg	Thr	Met	Phe	Asp	Val	Ile	Gly	Gly	Asn	Ala	Tyr	Thr
		195						200					205		
Ile	Gly	Gly	Arg	Ser	Arg	Cys	Ser	Ile	Gly	Phe	Ala	Val	Asn	Gly	Gly
		210						215					220		
Phe	Ile	Thr	Ala	Gly	His	Cys	Gly	Arg	Thr	Gly	Ala	Thr	Thr	Ala	Asn
		225						230					235		240
Pro	Thr	Gly	Thr	Phe	Ala	Gly	Ser	Ser	Phe	Pro	Gly	Asn	Asp	Tyr	Ala
				245						250				255	
Phe	Val	Arg	Thr	Gly	Ala	Gly	Val	Asn	Leu	Leu	Ala	Gln	Val	Asn	Asn
				260						265				270	
Tyr	Ser	Gly	Gly	Arg	Val	Gln	Val	Ala	Gly	His	Thr	Ala	Ala	Pro	Val
		275						280					285		
Gly	Ser	Ala	Val	Cys	Arg	Ser	Gly	Ser	Thr	Thr	Gly	Trp	His	Cys	Gly
		290						295				300			
Thr	Ile	Thr	Ala	Leu	Asn	Ser	Ser	Val	Thr	Tyr	Pro	Glu	Gly	Thr	Val
		305						310				315			320
Arg	Gly	Leu	Ile	Arg	Thr	Thr	Val	Cys	Ala	Glu	Pro	Gly	Asp	Ser	Gly
				325						330				335	
Gly	Ser	Leu	Leu	Ala	Gly	Asn	Gln	Ala	Gln	Gly	Val	Thr	Ser	Gly	Gly
				340						345				350	
Ser	Gly	Asn	Cys	Arg	Thr	Gly	Gly	Thr	Thr	Phe	Phe	Gln	Pro	Val	Asn
		355						360					365		
Pro	Ile	Leu	Gln	Ala	Tyr	Gly	Leu	Arg	Met	Ile	Thr	Thr	Asp	Ser	Gly
		370						375					380		
Ser	Ser	Pro	Ala	Pro	Ala	Pro	Thr	Ser	Cys	Thr	Gly	Tyr	Ala	Arg	Thr
		385								395				400	
Phe	Thr	Gly	Thr	Leu	Ala	Ala	Gly	Arg	Ala	Ala	Ala	Gln	Pro	Asn	Gly
				405						410				415	
Ser	Tyr	Val	Gln	Val	Asn	Arg	Ser	Gly	Thr	His	Ser	Val	Cys	Leu	Asn
				420						425				430	
Gly	Pro	Ser	Gly	Ala	Asp	Phe	Asp	Leu	Tyr	Val	Gln	Arg	Trp	Asn	Gly
		435						440					445		
Ser	Ser	Trp	Val	Thr	Val	Ala	Gln	Ser	Thr	Ser	Pro	Gly	Ser	Asn	Glu
		450						455				460			
Thr	Ile	Thr	Tyr	Arg	Gly	Asn	Ala	Gly	Tyr	Tyr	Arg	Tyr	Val	Val	Asn
		465						470			475				480
Ala	Ala	Ser	Gly	Ser	Gly	Ala	Tyr	Thr	Met	Gly	Leu	Thr	Leu	Pro	
				485						490				495	

<210> 7
 <211> 467
 <212> PRT

<213> Cellulomonas strain 69B4

<400> 7

```
Asn Glu Pro Ala Pro Pro Gly Ser Ala Ser Ala Pro Pro Arg Leu Ala
1      5      10      15
Glu Lys Leu Asp Pro Asp Leu Leu Glu Ala Met Glu Arg Asp Leu Gly
20      25      30
Leu Asp Ala Glu Glu Ala Ala Ala Thr Leu Ala Phe Gln His Asp Ala
35      40      45
Ala Glu Thr Gly Glu Ala Leu Ala Glu Glu Leu Asp Glu Asp Phe Ala
50      55      60
Gly Thr Trp Val Glu Asp Asp Val Leu Tyr Val Ala Thr Thr Asp Glu
65      70      75      80
Asp Ala Val Glu Glu Val Glu Gly Glu Gly Ala Thr Ala Val Thr Val
85      90      95
Glu His Ser Leu Ala Asp Leu Glu Ala Trp Lys Thr Val Leu Asp Ala
100     105     110
Ala Leu Glu Gly His Asp Asp Val Pro Thr Trp Tyr Val Asp Val Pro
115     120     125
Thr Asn Ser Val Val Val Ala Val Lys Ala Gly Ala Gln Asp Val Ala
130     135     140
Ala Gly Leu Val Glu Gly Ala Asp Val Pro Ser Asp Ala Val Thr Phe
145     150     155     160
Val Glu Thr Asp Glu Thr Pro Arg Thr Met Phe Asp Val Ile Gly Gly
165     170     175
Asn Ala Tyr Thr Ile Gly Gly Arg Ser Arg Cys Ser Ile Gly Phe Ala
180     185     190
Val Asn Gly Gly Phe Ile Thr Ala Gly His Cys Gly Arg Thr Gly Ala
195     200     205
Thr Thr Ala Asn Pro Thr Gly Thr Phe Ala Gly Ser Ser Phe Pro Gly
210     215     220
Asn Asp Tyr Ala Phe Val Arg Thr Gly Ala Gly Val Asn Leu Leu Ala
225     230     235     240
Gln Val Asn Asn Tyr Ser Gly Gly Arg Val Gln Val Ala Gly His Thr
245     250     255
Ala Ala Pro Val Gly Ser Ala Val Cys Arg Ser Gly Ser Thr Thr Gly
260     265     270
Trp His Cys Gly Thr Ile Thr Ala Leu Asn Ser Ser Val Thr Tyr Pro
275     280     285
Glu Gly Thr Val Arg Gly Leu Ile Arg Thr Thr Val Cys Ala Glu Pro
290     295     300
Gly Asp Ser Gly Gly Ser Leu Leu Ala Gly Asn Gln Ala Gln Gly Val
305     310     315     320
Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr Gly Gly Thr Thr Phe Phe
325     330     335
Gln Pro Val Asn Pro Ile Leu Gln Ala Tyr Gly Leu Arg Met Ile Thr
340     345     350
Thr Asp Ser Gly Ser Ser Pro Ala Pro Ala Pro Thr Ser Cys Thr Gly
355     360     365
Tyr Ala Arg Thr Phe Thr Gly Thr Leu Ala Ala Gly Arg Ala Ala Ala
370     375     380
Gln Pro Asn Gly Ser Tyr Val Gln Val Asn Arg Ser Gly Thr His Ser
385     390     395     400
Val Cys Leu Asn Gly Pro Ser Gly Ala Asp Phe Asp Leu Tyr Val Gln
405     410     415
Arg Trp Asn Gly Ser Ser Trp Val Thr Val Ala Gln Ser Thr Ser Pro
```

420 425 430
 Gly Ser Asn Glu Thr Ile Thr Tyr Arg Gly Asn Ala Gly Tyr Tyr Arg
 435 440 445
 Tyr Val Val Asn Ala Ala Ser Gly Ser Gly Ala Tyr Thr Met Gly Leu
 450 455 460
 Thr Leu Pro
 465

<210> 8
 <211> 189
 <212> PRT
 <213> Cellulomonas spp.

<400> 8

Phe Asp Val Ile Gly Gly Asn Ala Tyr Thr Ile Gly Gly Arg Ser Arg
 1 5 10 15
 Cys Ser Ile Gly Phe Ala Val Asn Gly Gly Phe Ile Thr Ala Gly His
 20 25 30
 Cys Gly Arg Thr Gly Ala Thr Thr Ala Asn Pro Thr Gly Thr Phe Ala
 35 40 45
 Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Phe Val Arg Thr Gly Ala
 50 55 60
 Gly Val Asn Leu Leu Ala Gln Val Asn Asn Tyr Ser Gly Gly Arg Val
 65 70 75 80
 Gln Val Ala Gly His Thr Ala Ala Pro Val Gly Ser Ala Val Cys Arg
 85 90 95
 Ser Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile Thr Ala Leu Asn
 100 105 110
 Ser Ser Val Thr Tyr Pro Glu Gly Thr Val Arg Gly Leu Ile Arg Thr
 115 120 125
 Thr Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Leu Ala Gly
 130 135 140
 Asn Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr
 145 150 155 160
 Gly Gly Thr Thr Phe Phe Gln Pro Val Asn Pro Ile Leu Gln Ala Tyr
 165 170 175
 Gly Leu Arg Met Ile Thr Thr Asp Ser Gly Ser Ser Pro
 180 185

<210> 9
 <211> 28
 <212> PRT
 <213> Cellulomonas strain 69B4

<400> 9

Met Thr Pro Arg Thr Val Thr Arg Ala Leu Ala Val Ala Thr Ala Ala
 1 5 10 15
 Ala Thr Leu Leu Ala Gly Gly Met Ala Ala Gln Ala
 20 25

<210> 10
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>

<223> primer

<220>

<221> misc_feature

<222> (3)..(3)

<223> n is a, c, g, or t

<400> 10

acnacsggst ggcrgtgcgg cac

23

<210> 11

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<220>

<221> misc_feature

<222>